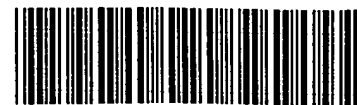*1646*

IFWO

RAW SEQUENCE LISTING   DATE: 01/21/2004
PATENT APPLICATION: **US/10/645,702**   TIME: 12:30:15

Input Set : **N:\Crf3\RULE60\10645702.RAW.txt**
Output Set: **N:\CRF4\01212004\J645702.raw**

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 1 <110> APPLICANT: Shi, Yanggu
 2        Ruben, Steve M.
 3 <120> TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
 4 <130> FILE REFERENCE: PF398P2
 5 <140> CURRENT APPLICATION NUMBER: 10/645,702
 6 <141> CURRENT FILING DATE: 2003-08-22
 7 <150> PRIOR APPLICATION NUMBER: US/09/796,844
 8 <151> PRIOR FILING DATE: 2001-03-02
 9 <150> PRIOR APPLICATION NUMBER: 60/187,015
10 <151> PRIOR FILING DATE: 2000-03-06
11 <150> PRIOR APPLICATION NUMBER: PCT/US00/05759
12 <151> PRIOR FILING DATE: 2000-03-06
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/21048
14 <151> PRIOR FILING DATE: 1999-09-15
15 <150> PRIOR APPLICATION NUMBER: 09/268,311
16 <151> PRIOR FILING DATE: 1999-03-16
17 <150> PRIOR APPLICATION NUMBER: PCT/US98/19121
18 <151> PRIOR FILING DATE: 1998-09-16
19 <150> PRIOR APPLICATION NUMBER: 09/154,219
20 <151> PRIOR FILING DATE: 1998-09-16
21 <150> PRIOR APPLICATION NUMBER: 60/059,133
22 <151> PRIOR FILING DATE: 1997-09-17
23 <160> NUMBER OF SEQ ID NOS: 35
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1816
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (10)..(1287)
33 <221> NAME/KEY: mat_peptide
34 <222> LOCATION: (67)..(1287)
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W--> 35 `<221> sig_peptide`
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36 <222> LOCATION: (10)..(66)
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W--> 37 `<400> 1`
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38       gcacgagcg atg tcg ctc gtg ctg cta agc ctg gcc gcg ctg tgc agg agc 51
39                 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser
40                                -15                    -10
41       gcc gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca 99
42       Ala Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro
43        -5              -1  1              5                      10
44       tct cca gag tgg atg cta caa cat gat cta atc ccc gga gac ttg agg 147
```

ENTERED

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45    Ser Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg
46                    15                  20                  25
47    gac ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat    195
48    Asp Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr
49                    30                  35                  40
50    tca att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc    243
51    Ser Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile
52              45                  50                  55
53    cgc ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc    291
54    Arg Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe
55        60                  65                  70                  75
56    cag tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act    339
57    Gln Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr
58                    80                  85                  90
59    cag acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tac atc ggc ttc    387
60    Gln Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe
61                    95                 100                 105
62    cct gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct    435
63    Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro
64                   110                 115                 120
65    aat gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc    483
66    Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr
67              125                 130                 135
68    tca cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc ,  531
69    Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val
70    140                 145                 150                 155
71    aag gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat    579
72    Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn
73                   160                 165                 170
74    gag gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga    627
75    Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg
76                   175                 180                 185
77    tac atg gct ctt atc caa cac agc act atc atc ggg ttt tct cag gtg    675
78    Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val
79              190                 195                 200
80    ttt gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca    723
81    Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro
82        205                 210                 215
83    gtg act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt    771
84    Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe
85    220                 225                 230                 235
86    cct act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt gtg ctc    819
87    Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu
88              240                 245                 250
89    tgc cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag    867
90    Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys
91              255                 260                 265
92    ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca    915
93    Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr
```

RAW SEQUENCE LISTING   DATE: 01/21/2004
PATENT APPLICATION: US/10/645,702   TIME: 12:30:15

Input Set : N:\Crf3\RULE60\10645702.RAW.txt
Output Set: N:\CRF4\01212004\J645702.raw

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 94            270                 275                 280       .
 95   tgg gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc   963
 96   Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile
 97        285                 290                 295
 98   aag aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt  1011
 99   Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val
100     300                 305                 310                 315
101    ctt gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac  1059
102    Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr
103                    320                 325                 330
104    ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa  1107
105    Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu
106             335                 340                 345
107    aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt  1155
108    Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu
109           350                 355                 360
110    gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat  1203
111    Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn
112      365                 370                 375
113    gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt  1251
114    Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser
115    380                 385                 390                 395
116    ccc agt gag aac tct caa gac tct tcc cct tgc ctt taacctttc       1297
117    Pro Ser Glu Asn Ser Gln Asp Ser Ser Pro Cys Leu
118             .          400                 405
119    tgcagtgatc taagaagcca gattcatctg cacaaatacg tggtggtcta ctttagagag 1357
120    attgatacaa aagacgatta caatgctctc agtgtctgcc ccaagtacca cctcatgaag 1417
121    gatgccactg ctttctgtgc agaacttctc catgtcaagt agcaggtgtc agcaggaaaa 1477
122    agatcacaag cctgccacga tggctgctgc tccttgtagc ccacccatga gaagcaagwg 1537
123    accttaaagg cttcctatcc caccaattac agggaaaaaa cgtgtgatga tcctgaagct 1597
124    tactatgcag cctacaaaca gccttagtaa ttaaaacatt ttataccaat aaaattttca 1657
125    aatattgcta actaatgtag cattaactaa cgattggaaa ctacatttac aacttcaaag 1717
126    ctgttttata catagaaatc aattacagtt ttaattgaaa actataacca ttttgataat 1777
127    gcaacaataa agcatcttca gccaaaaaaa aaaaaaaaa                        1816
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 426
131 <212> TYPE: PRT
132 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
134    Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
135                    -15                 -10                 -5
136    Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
137            -1   1              5                  10
138    Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
139          15                  20                  25
140    Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
141    30                  35                  40                  45
142    Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
143                    50                  55                  60 .
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RAW SEQUENCE LISTING   DATE: 01/21/2004
PATENT APPLICATION: US/10/645,702   TIME: 12:30:15

Input Set : N:\Crf3\RULE60\10645702.RAW.txt
Output Set: N:\CRF4\01212004\J645702.raw

```
144    Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
145                65                  70                  75
146    Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
147            80                  85                  90
148    Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
149        95                  100                 105
150    Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
151    110                 115                 120                 125
152    Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
153                130                 135                 140
154    Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
155                145                 150                 155
156    Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
157            160                 165                 170
158    Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
159        175                 180                 185
160    Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
161    190                 195                 200                 205
162    Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
163                210                 215                 220
164    Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
165                225                 230                 235
166    Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
167            240                 245                 250
168    Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
169        255                 260                 265
170    Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
171    270                 275                 280                 285
172    Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
173                290                 295                 300
174    Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
175            305                 310                 315
176    Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
177        320                 325                 330
178    Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
179        335                 340                 345
180    Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
181    350                 355                 360                 365
182    Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
183                370                 375                 380
184    Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
185            385                 390                 395
186    Glu Asn Ser Gln Asp Ser Ser Pro Cys Leu
187            400                 405
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 426
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 3
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194        Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
195         1               5                   10                  15
196        Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
197                         20                  25                  30
198        Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
199                 35                  40                  45
200        Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
201             50                  55                  60
202        Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
203         65                  70                  75                  80
204        Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
205                     85                  90                  95
206        Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
207                 100                 105                 110
208        Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
209                 115                 120                 125
210        Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
211             130                 135                 140
212        Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
213         145                 150                 155                 160
214        Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
215                 165                 170                 175
216        Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
217                 180                 185                 190
218        Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
219                 195                 200                 205
220        Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
221             210                 215                 220
222        Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
223         225                 230                 235                 240
224        Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
225                 245                 250                 255
226        Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
227                 260                 265                 270
228        Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
229                 275                 280                 285
230        Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
231             290                 295                 300
232        Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
233         305                 310                 315                 320
234        Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
235                 325                 330                 335
236        Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
237                 340                 345                 350
238        Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
239                 355                 360                 365
240        Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
241             370                 375                 380
242        Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/21/2004
PATENT APPLICATION: US/10/645,702   TIME: 12:30:16

Input Set : N:\Crf3\RULE60\10645702.RAW.txt
Output Set: N:\CRF4\01212004\J645702.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 17,65,148,160,362,373,388,406
Seq#:5; N Pos. 10,39,42,44,45,53,106,120,121,128,163,173,210,223,233,238
Seq#:5; N Pos. 241,247,251,261,267,269,274,277,279,280,285,289,293,295,302
Seq#:5; N Pos. 305,312
Seq#:17; N Pos. 29,101

VERIFICATION SUMMARY   DATE: 01/21/2004
PATENT APPLICATION: **US/10/645,702**   TIME: 12:30:16

Input Set : **N:\Crf3\RULE60\10645702.RAW.txt**
Output Set: **N:\CRF4\01212004\J645702.raw**

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L:35  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:260 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:266 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:269 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:272 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:275 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:298 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:304 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:307 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:310 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:319 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:325 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
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L:331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:334 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:343 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:346 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:352 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
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L:364 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
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L:370 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:373 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:376 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:379 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:382 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:483 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:486 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:758 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:760 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
```